



UNICLANTS SPINS (De Entered)

REPORT DOCUMENTATION PAGE

18. SUPPLEMENTARY NOTES

J. Appl. Prob. V 17, 25-32, 1980

19. KEY WORDS (Continue on reverse side if necessary and identify by block number)

Simple batch epidemic process; limiting distributions; marginal distribution

20. ABSTRACT (Continue on reverse side if necessary and identify by block number)

A simple epidemic process in which the number of individuals who can become infected at any point in time is itself a random variable is described. The descrete asymptotic behaviour of such a process is discussed. In particular, the associated marginal distribution of the limiting process is considered.

JOB

DD 1 JAN 73 1473

EDITION OF 1 NOV 65 IS OBSOLETE

400217

UNCLASSIFIED

SECURITY CLASSIFICATION OF THIS PAGE (When Date Entered)

READ INSTRUCTIONS

BEFORE COMPLETING FORM RECIPIENT'S CATALOG NUMBER

TYPE OF REPORT & PERIOD COVERED

J. Appl. Prob. 17, 25-32 (1980)
Printed in Israel
0021-9002/80/010025-08 \$01.05

© Applied Probability Trust 1980

THE DISCRETE ASYMPTOTIC BEHAVIOUR OF A SIMPLE BATCH EPIDEMIC PROCESS

L BILLARD,"

H. LACAYO"

N. A. LANGBERG. Florida State University

Abstract

A simple epidemic process in which the number of individuals who can become infected at any point in time is itself a random variable is described. The discrete asymptotic behaviour of such a process is discussed. In particular, the associated marginal distribution of the limiting process is considered.

SIMPLE BATCH EPIDENIC PROCESS; LIMITING DISTRIBUTIONS; MARGINAL DISTRIBUTION

1. Introduction

A simple epidemic process in a closed population consists of susceptible individuals who may become infective individuals. Suppose initially there are N susceptibles and a infectives. Recently, Billard, Lacayo and Langberg (1979) showed how this process may be described in terms of N independent exponential random variables representing the times between any two successive occurrences of a new infective.

In this work, the following extension of the simple epidemic process is considered. When occurrences of infectives in the simple epidemic model are viewed as realizations of a jump process, each jump is of fixed size one. However, more generally, the size of the jumps may be a random variable. For descriptive reasons, we call this extension a simple batch epidemic process.

Our purpose is to investigate the asymptotic behaviour of a sequence of simple batch epidemic processes when the population size N goes to infinity. Before obtaining the main results, we elaborate and introduce some notation.

AFOSR 18-3618

25

Approved for public release; distribution unlimited.

Received 14 July 1978; revision received 23 January 1979.

Postal address for all authors: Department of Statistics and Statistical Consulting Center, The Plorida State University, Tallahussee, Florida 32306, U.S.A.

^{*} Research supported by National Institutes of Health Grant No. 1. RO1 GM26651-01.

^{*} Research supported by Air Force Office of Scientific Research AFSC, USAF, under Grant APOSR 74-2581D.

^{*} Research Supported by Air Force Office of Scientific Research AFSC, USAF, under Grant APOSR 76-3109.

2. A simple batch epidemic model

Let the size of the jumps be represented by the sequence of random variables Z_h $i=1,2,\cdots$, with Z_i taking values $\{1,2,\cdots\}$. That is, Z_i is the number of individuals becoming infected at the *i*th occurrence of infection. Then, the number of jumps that has occurred until at least k of the susceptible individuals are infected, is R(k) given by

(1)
$$R(k) = \min \left\{ r \middle| \sum_{j=1}^{r} Z_j \ge k \right\}, \qquad k = 1, \dots, N.$$

Clearly, $1 \le R(k) \le k$. If D_i is the total number of new individuals who have become infected just before the *i*th jump, it follows that

(2)
$$D_{i} = \begin{cases} 0, & i = 1, \\ \sum_{i=1}^{i-1} Z_{i}, & i = 2, \dots, R(N), \end{cases}$$

where initially there are a infectives. Thus (2) implies that after the ith jump $\{0 \le i \le R(N) - 1\}$ there are $(D_{i+1} + a)$ infectives, and after the R(N)th jump, there are (N + a) infectives. For convenience, we take a = 1.

We recall that in the simple epidemic process (where $Z_i = 1$ always), the interinfection time T_i between the (i-1)th and ith occurrence of a new infective is exponentially distributed with parameter proportional to i(N+1-i). However, in the present case, since the jump sizes are themselves random variables, the conditional mean (interinfection) time is also a random variable. Therefore, let us define the realizations of the random variable $\mu(N, D_i)$, $i = 1, \dots, R(N)$, as the mean time between the occurrence of the (i-1)th and ith jump, that is, $E(T_i)$.

We may now define the interinfection time between the (i-1)th and ith jump as $T_i = \mu(N, D_i)U_h$, $i = 1, \dots, R(N)$, where the U_h , $i = 1, \dots, R(N)$, are independent exponentially distributed random variables with mean one, and where the U_i are independent of the Z_h , $j = 1, 2, \dots$. It follows immediately that the total time until there are at least k new infectives, S_h , may be written as

(3)
$$S_k = \sum_{i=1}^{R(k)} \mu(N, D_i) U_i, \quad k = 1, \dots, R(N).$$

We note that the particular case $S_{R(N)} = S_N$ is simply the duration time of the simple batch epidemic process.

Finally, we denote the total number of new infectives present at time t by $X_N(t)$, t>0, with realizations $0, \dots, N$. Then, for every set of positive real numbers t_i , $j=1,\dots,m$ and a corresponding set of positive integers k_n , $j=1,\dots,m$, we have the relationship

AIR FORCE OFFICE OF SCIENTIFIC RESEARCH (AFSC)
NOTICE OF TRANSMITTAL TO DDC
This technical report has been reviewed and is
approved for public release IAW AFR 190-12 (7b).
Astribution is unlimited.
A. D. BLOSE
Lechnical Information Officer

(4)
$$P\{X_N(t_j) \ge k_j, j = 1, \dots, m\} = P\{S_{k_j} \le t_j, j = 1, \dots, m\}.$$

Hence, it follows that the simple batch epidemic process is uniquely determined by the $\mu(N, D_i)$, $i = 1, \dots, R(N)$, and the Z_i , $i = 1, 2, \dots$

In Section 3, we present a condition which is sufficient to ensure the convergence in law of a sequence of such processes to a discrete stochastic process. In Sections 4 and 5, some specific marginal distributions of X(t) are investigated.

3. Convergence in law of a sequence of simple batch epidemics

Let X(t), t > 0, be a stochastic counting process. Let there be associated with X(t) the random variables $\mu(D_i)$ where

(5)
$$D_{i} = \begin{cases} 0, & i = 1, \\ \sum_{j=1}^{i-1} Z_{j}, & i = 2, 3, \dots, \end{cases}$$

with the Z_i being the jump random variables defined in the previous section.

Let $X_N(t)$, t>0, $N=1,2,\cdots$; be a sequence of simple batch epidemics as defined in the previous section. On the array of functions $\mu(N,D_i)$, $i=1,\cdots,R(N)$, $N=1,2,\cdots$, we impose the following condition. For each value of i,

(6)
$$\lim_{N\to\infty}\mu(N,D_i)=\mu(D_i)\,a.s.$$

where $\mu(D_i)$, $i = 1, 2, \dots$, is a finite positive function. One such family of double arrays of mean interinfection times satisfying (6) is

(7)
$$\mu(N, D_i) = cN^{\alpha}(N - D_i)^{-\alpha}(D_i + 1)^{-\beta}, \quad i = 1, \dots, R(N), N = 1, 2, \dots,$$

where α , β , and c are positive quantities. This family may be viewed as a generalisation of that suggested by Severo (1969). Another particular case is the model of McNeil (1972).

Let the waiting times between the (i-1)th and ith jump be $T_i = \mu(D_i)U_h$ $i=1,2,\cdots$, where as before the U_i are independent exponentially distributed random variables with mean one, and are independent of the Z_h $j=1,2,\cdots$. Finally, let us define

(8)
$$S'_k = \sum_{i=1}^{R(k)} \mu(D_i)U_i, \quad k = 1, 2, \dots,$$

where R(k) is as defined in (1). Then, for any arbitrary but finite set of positive real numbers $i_j = 1, \dots, m$, and positive integers $k_j = 1, \dots, m$,

		•
Accession		For /
NTIS	GRA	1
DTIC TAB		ក
Unannounced		
Justification		ion
Ву		
Distributi		\a_
Availabil		
Dist	Avel Spe	and/or
A	20	

(9)
$$P\{X(t_i) \ge k_{j-1} = 1, \dots, m\} = P\{S'_{k_i} \le t_{j-1} = 1, \dots, m\}.$$

The following theorem may now be proved.

Theorem. Let $X_N(t)$, t>0, $N=1,2,\cdots$, be a sequence of simple batch epidemics as described by the quantities $\mu(N,D_i)$, $i=1,\cdots,R(N)$, and Z_n , $i=1,2,\cdots$. When the condition (6) holds, the joint and the marginal state probabilities of the $X_N(t)$ process converge to the corresponding state probabilities of the counting process X(t), t>0.

Proof. We prove the result for the joint state probabilities. The result for the marginal probabilities is proved analogously. It is sufficient to show that for every arbitrary but finite set of positive real numbers t_i , $j = 1, \dots, m$, and positive integers k_i , $j = 1, \dots, m$,

(10)
$$\lim_{M \to \infty} P\{X_N(t_j) \ge k_j, j = 1, \dots, m\} = P\{S'_{t_j} \le t_j, j = 1, \dots, m\}.$$

To prove (10), we recall that $R(k_i)$ is independent of N and is bounded above by k_i . The condition (6) implies that

$$\mu(N, D_i)U_i \xrightarrow{\text{a.s.}} \mu(D_i)U_i$$

Thus,

$$S_{k_i} = \sum_{i=1}^{R(k_i)} \mu(N, D_i) U_i \xrightarrow{a.k.} \sum_{i=1}^{R(k_i)} \mu(D_i) U_i = S'_{k_i}$$

for all $j = 1, \dots, m$. Therefore,

(11)
$$\lim_{n \to \infty} P\{S_{k_i} \le t_{j_i} j = 1, \dots, m\} = P\{S_{k_i} \le t_{j_i} j = 1, \dots, m\}.$$

Hence, combining (4) and (11), the result (10) follows.

We note that the exponentiality assumption of the interinfection times as well as the independence between the U_i and the Z_i $i = 1, 2, \dots$, were not necessary to prove the theorem. Thus, this theorem may be applied to more general situations.

4. Distribution of the limiting epidemic process

In this section, a study of the marginal distribution of X(t) is made. In epidemic theory, this corresponds to the distribution of the number of new infectives for a large population. It follows that

$$P\{X(t) \ge k\} = P\left\{\sum_{i=1}^{R(k)} \mu(D_i)U_i \le t\right\}$$

$$= \sum_{i=1}^{k} P\left\{\sum_{i=1}^{k} \mu(D_i)U_i \le t \mid R(k) = \nu\right\} P\{R(k) = \nu\}.$$
(12)

Clearly, we may write

$$P\{R(k) = \nu\} = P\left(\sum_{i=1}^{\nu-1} Z_i < k, \sum_{i=1}^{\nu} Z_i \ge k\right)$$

and if the Z_i are independent random variables

(13)
$$P\{R(k) = \nu\} = \sum_{m=\nu-1}^{k-1} P\left(\sum_{i=1}^{\nu-1} Z_i = m\right) P(Z_{\nu} \ge k - m).$$

Therefore, when the Z_i are identically distributed, this probability (13) can be easily evaluated.

The conditional probability term of (12) may be written as

$$P\left\{\sum_{i=1}^{r} \mu(D_i)U_i \le t \,\middle|\, R(k) = \nu\right\}$$

$$= \sum_{k \in \mathbb{Z}} P\left\{\sum_{i=1}^{r} \mu(D_i)U_i \le t \,\middle|\, R(k) = \nu, Z = z\right\} P(Z = z),$$
(14)

where $z = (z_1, \dots, z_r)$ is a particular realization of a set of jump statistics $Z = (Z_1, \dots, Z_r)$ and where

$$Z = \left\{ z : \sum_{i=1}^{n-1} z_i < k \quad \text{and} \quad \sum_{i=1}^{n} z_i \ge k \right\}.$$

If the Z_i are independent identically distributed random variables,

(15)
$$P(Z=z) = \prod_{i=1}^{n} P(Z=z_i).$$

To evaluate the remaining term in (14), it is noted that for given R(k) and Z, the actual jump sizes at each stage are known. Hence, the distribution of $\mu(D_i)U_i$ is known for each $i=1,\dots,\nu$. If the parameters $\mu(D_i)$, $i=1,\dots,\nu$, are distinct, an application of Billard, Lacayo and Langberg (1979), Theorem 1 yields the desired solution; whilst if the parameters $\mu(D_i)$, $i=1,\dots,\nu$, are not distinct the solution follows from an application of Billard, Lacayo and Langberg (1980), Theorem 2. Thus, we obtain the distribution function from (12) and hence the probability distribution of the number of infectives.

Although we have restricted our attention here to the marginal distribution of X(t), we note that an explicit form for the finite-dimensional joint distribution of

the process $\{X(t_i), j=1,\dots,m\}$ can be easily studied by generalizing (12), (13) and (14).

5. Examples

There are some particular cases worthy of special attention. Consider first the distribution of R(k). Suppose that the random variables $(Z_i - 1)$ are independent and follow a Poisson distribution with parameter λ . That is,

$$P\{Z=z+1\}=e^{-\lambda}\lambda^{z}/z!, z=0,1,\cdots$$

Then, from (13) it can be shown that

$$P\{R(k) = \nu\} = \sum_{m=\nu-1}^{k-1} \sum_{r=k-m-1}^{m} e^{-\lambda \nu} \lambda^{m+r-\nu+1} (\nu-1)^{m-\nu+1} / [r! (m-\nu+1)!]$$
(16) = $q(\nu)$, say.

Another example of jump processes is when the Z_i are independent random variables taking values 1 or 2 with probability p or q, respectively. This corresponds to the case in which individuals can become infected in batches of one or two only. Then,

$$P\{R(k) = \nu\} = P\left\{\sum_{i=1}^{\nu-1} Z_i = k-1, Z_{\nu} = 1 \text{ or } 2\right\} + P\left\{\sum_{i=1}^{\nu-1} Z_i = k-2, Z_{\nu} = 2\right\}$$

$$= \binom{\nu}{k-\nu} p^{2\nu-k-1} q^{k-\nu} (2\nu - kq - \nu p)/\nu.$$

Let us now consider special forms for the quantity $\mu(D_i)$. One particular case is when

$$\mu(D_i) = \lim_{n \to \infty} \mu(N, D_i) = \lim_{n \to \infty} N^*(N - D_i)^{-*}(mi)^{-*},$$

where α , $\beta > 0$ and where $m = E(Z_1) > 0$. That is,

(18)
$$\mu(D_i) = (mi)^{-\theta}.$$

The equation (12) gives

$$P\{X(t) \ge k\} = \sum_{i=1}^{k} P\left\{\sum_{i=1}^{\nu} (mi)^{-\rho} U_i \le t \, \middle| \, R(k) = \nu\right\} P\{R(k) = \nu\},$$

and for $\beta = 1$,

(19)
$$P\{X(t) \ge k\} = \sum_{\nu=1}^{k} P\left\{\sum_{i=1}^{\nu} i^{-1}U_{i} \le mt\right\} \cdot P\{R(k) = \nu\},$$
$$= \sum_{\nu=1}^{k} (1 - e^{-mt})^{\nu} P\{R(k) = \nu\}$$

by an application of Billard, Lacayo and Langberg (1979), Theorem 1.

In some populations, if N is sufficiently large relative to the number of infectives, it is reasonable to expect that the infection rate is a constant independent of the number of infectives. That is,

(20)
$$\mu(D_i) = \lim_{N \to \infty} \mu(N, D_i) = c.$$

Then it follows that

$$P\{X(t) \ge k\} = \sum_{\nu=1}^{k} P\left\{c \sum_{i=1}^{\nu} U_i \le t \, \middle| \, R(k) = \nu\right\} P\{R(k) = \nu\}$$

$$= \sum_{\nu=1}^{k} P(W_{\nu} \le c^{-1}t) P\{R(k) = \nu\}$$
(21)

where \dot{W}_{ν} has a gamma distribution with parameters 1 and ν .

Finally, the quantity $\mu(D_i)$ may still be a random variable but also independent of the number of infectives. That is,

$$\mu(D_i) = D.$$

Then.

$$P\{X(t) \ge k\} = \sum_{\nu=1}^{k} P(Y = DW_{\nu} \le t)P\{R(k) = \nu\}$$

where W_r , follows a gamma distribution with parameters 1 and ν . For a given distribution D_r , this probability can be evaluated. For example, suppose D_r follows a Pareto distribution

$$f(d) = \alpha \beta^{\alpha} d^{-\alpha-1}, \quad d > \beta, \quad \alpha, \beta > 0.$$

Then, routine but lengthy derivation gives

(23)
$$P(Y \le t) = \Gamma^{-1}(\nu) \{ \gamma(\nu, t/\beta) - (\beta/t)^{\alpha} \gamma(\alpha + \nu, t/\beta) \},$$

where

$$\gamma(\lambda,\xi)=\int_0^{\xi}e^{-u}u^{\lambda-1}du$$

is the tabulated incomplete gamma function.

We note that we may write

$$X(t)=\sum_{i=0}^{N(t)}Z_{i}\qquad Z_{0}=0,$$

where N(t) is the number of jumps that have occurred up to time t. If $\mu(D_t) = c$, N(t) is a Poisson process with rate c^{-1} and thus, if the Z_t are independent and

identically distributed, X(t) is a compound Poisson process. If the $\mu(D_t)$ are independent and identically distributed, N(t) is a renewal process and thus, if the pairs $[Z_i, \mu(D_i)]$ are independent and identically distributed, X(t) is a renewal reward process (Ross (1970), p. 51), that is a special case of a cumulative process (Cox (1962), p. 91).

Acknowledgement

The authors wish to thank the referee for his very careful reading of the original manuscript and his helpful comments.

References

BILLARD, L., LACAYO, H. AND LANGBURG, N. (1979) A new look at the simple spidemic process. J. Appl. Prob. 16, 198-202.

BILLARD, L., LACAYO, H. AND LANGBURG, N. A. (1980) Generalizations of the simple epidemic process. J. Appl. Prob. 17(4).

Cox, D. R. (1962) Renewel Theory. Methuen, London.

McNan., D. R. (1972) On the simple stochastic epidemic. Biometrika 59, 494-497.
Ross, S. M. (1970) Applied Probability Medels with Optimization Applications. Holden-Day, San

SEVERO, N. C. (1969) Generalizations of some stochastic epidemic models. Math. Biosci. 4, 395-402.